



# **Interactions of Organophosphorus and Related Compounds with Acetylcholinesterase**

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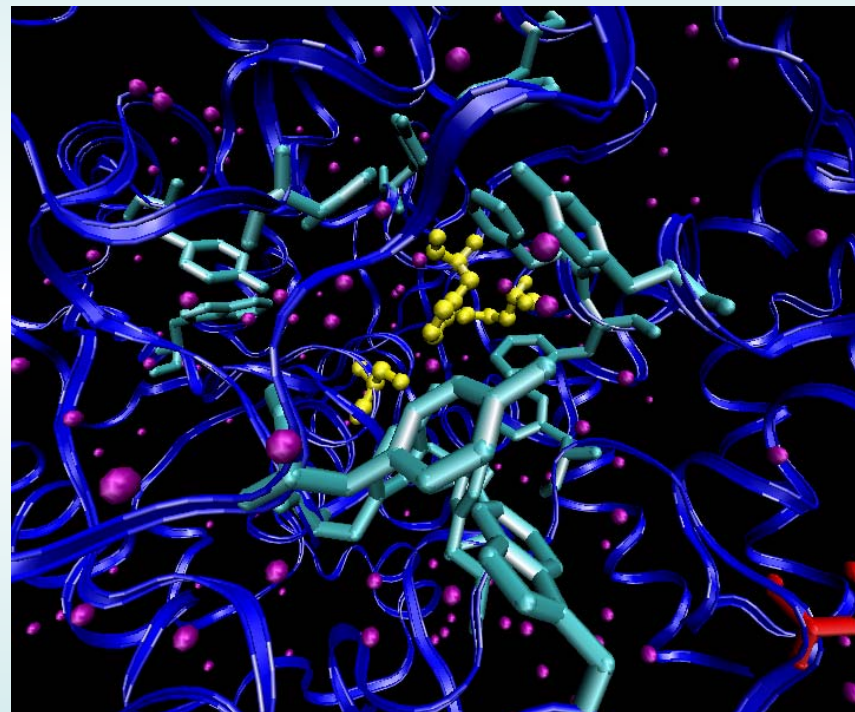
# Technical Goals



## Objectives: Understanding of :

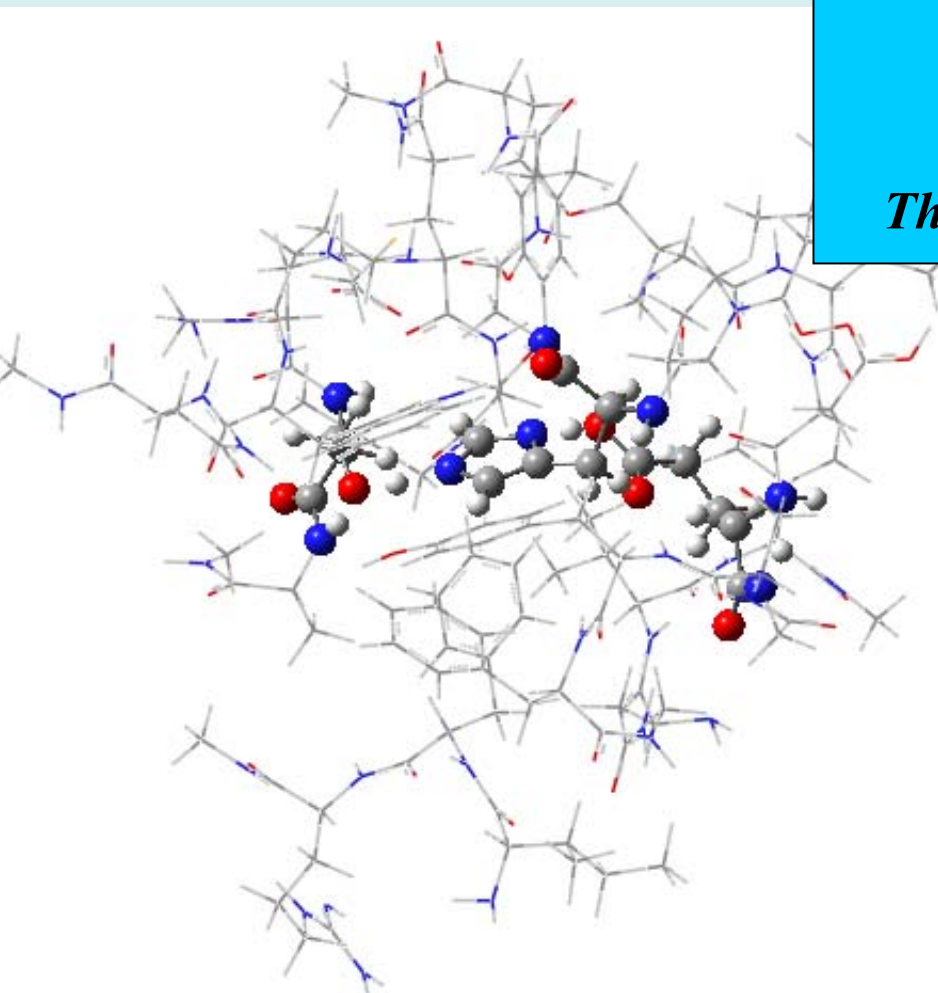
- reversible and irreversible binding by OP and other compounds in active site of acetylcholinesterase
- role of solvent
- mechanism of oxime therapy
- 'Aging' mechanism

by theoretical modeling to facilitate development of new compounds for therapeutics and prophylaxis.





# Previous Results



**AChE:**  
**Previous results used Mixed**  
**Quantum/Classical and QM/QM**  
**Modeling**  
***Theor. Chem. Acc. (2003) 1009:160-168***

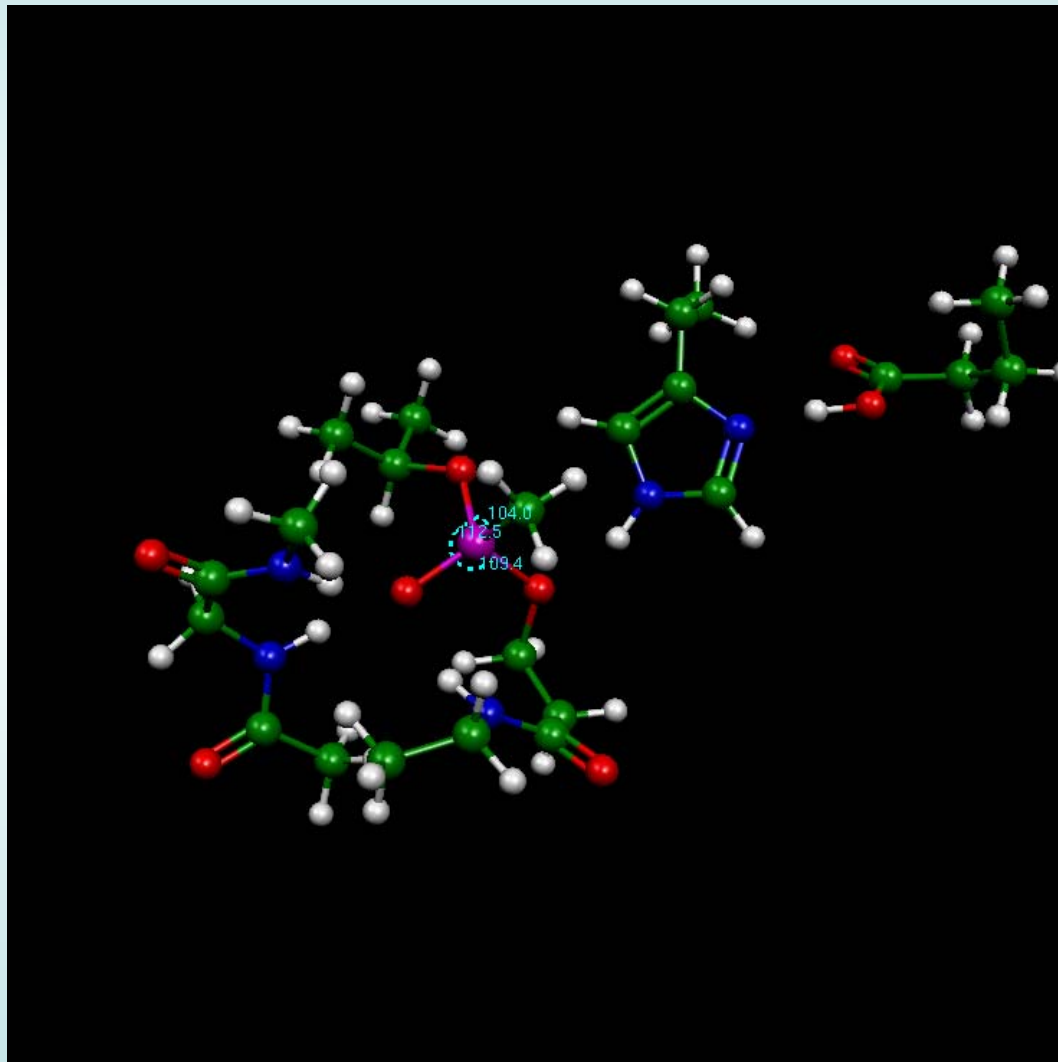
- Excellent alignment of catalytic triad
- Some sensitivity to algorithm (ONIOM vs SIMOMM), forcefield, model size
- ~15 kcal/mol TS barrier for OP binding
- QM/QM shows charge transfer between OP and oxyanion hole on binding
- Starting geometries taken from exptl data



# Organophosphate Family

B3LYP/3-21G

- Maintain strong bonding within catalytic triad
- Maintain H-bonding with Oxyanion Hole
- Tetrahedral intermediate without F- (LG)
- VERY Stable trig. bipyr. with F- (LG)
- Sarin, Soman, Tabun, DMMP, DFP, DEFP

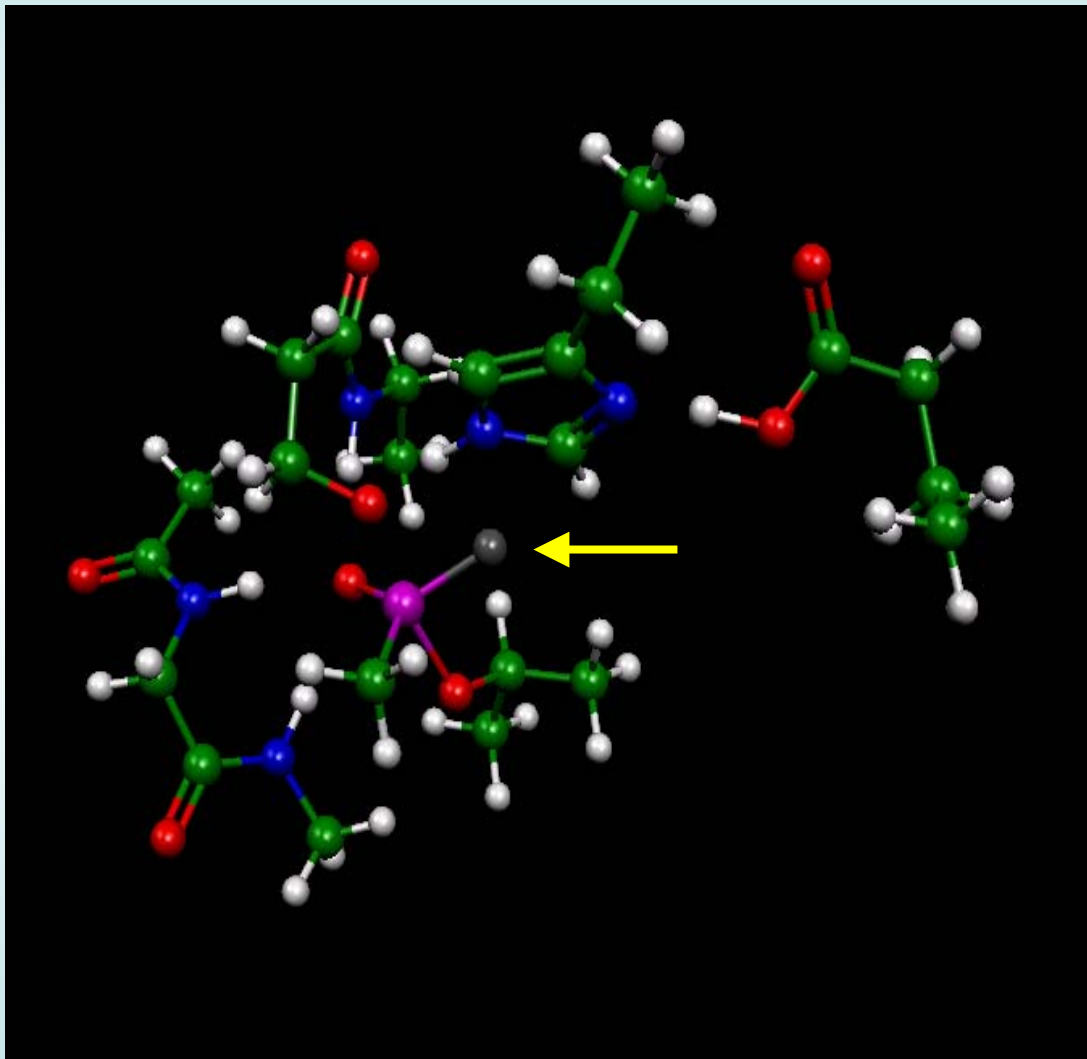


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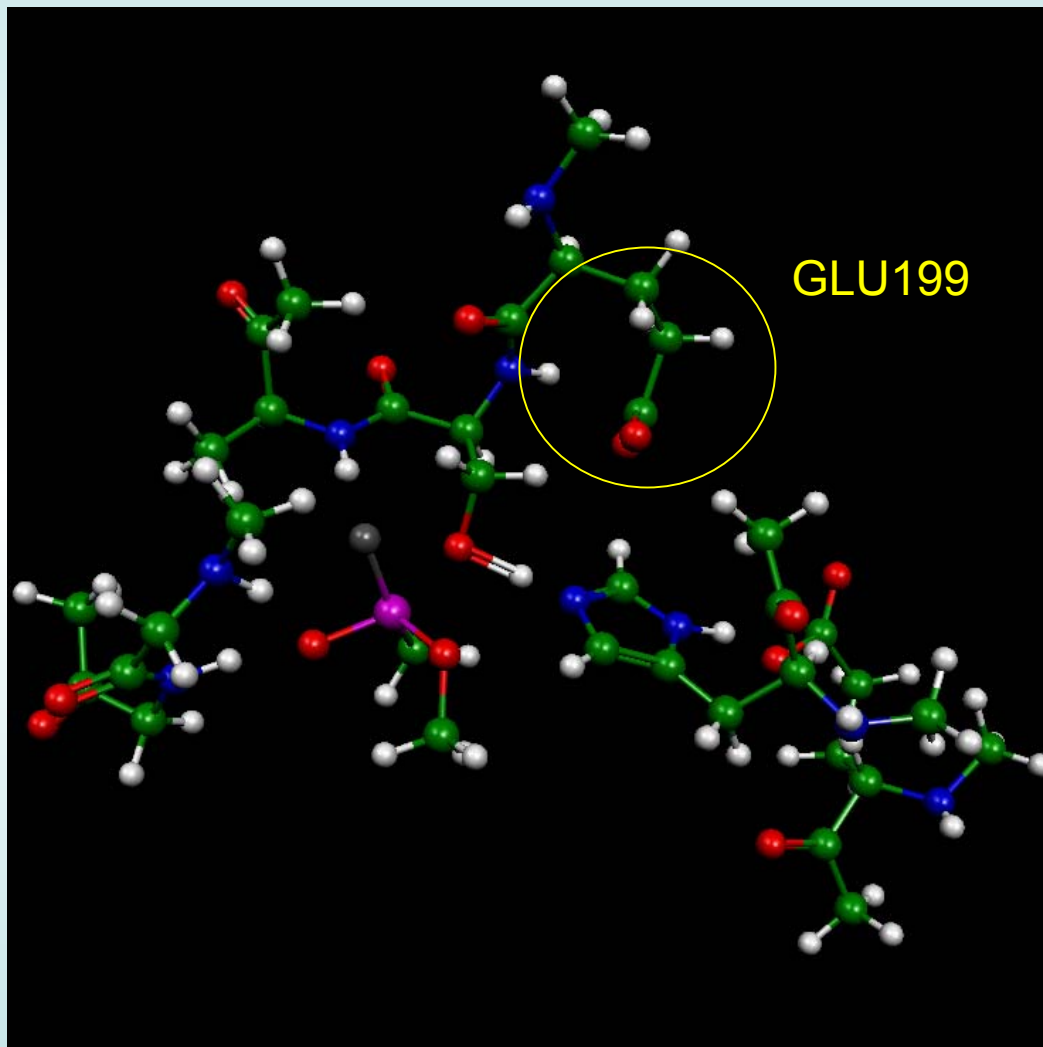
## Orientation and Structure



- Apical leaving group preferred.
- May bind with equatorial leaving group, product higher in energy by **10+ kcal/mol**
- Multiple minima WRT sidechain orientation, within **~3 kcal/mol** of each other



# Large Enough Yet?



B3LYP/3-21G

- Note GLU199 swinging over HIS to stabilize
- ***Additional*** H-bond to HIS and not ***alternative***, as per Kovach et al.
- Bonding to oxyanion hole (OX) maintained
- LG intact, alternative H-bond w/OX

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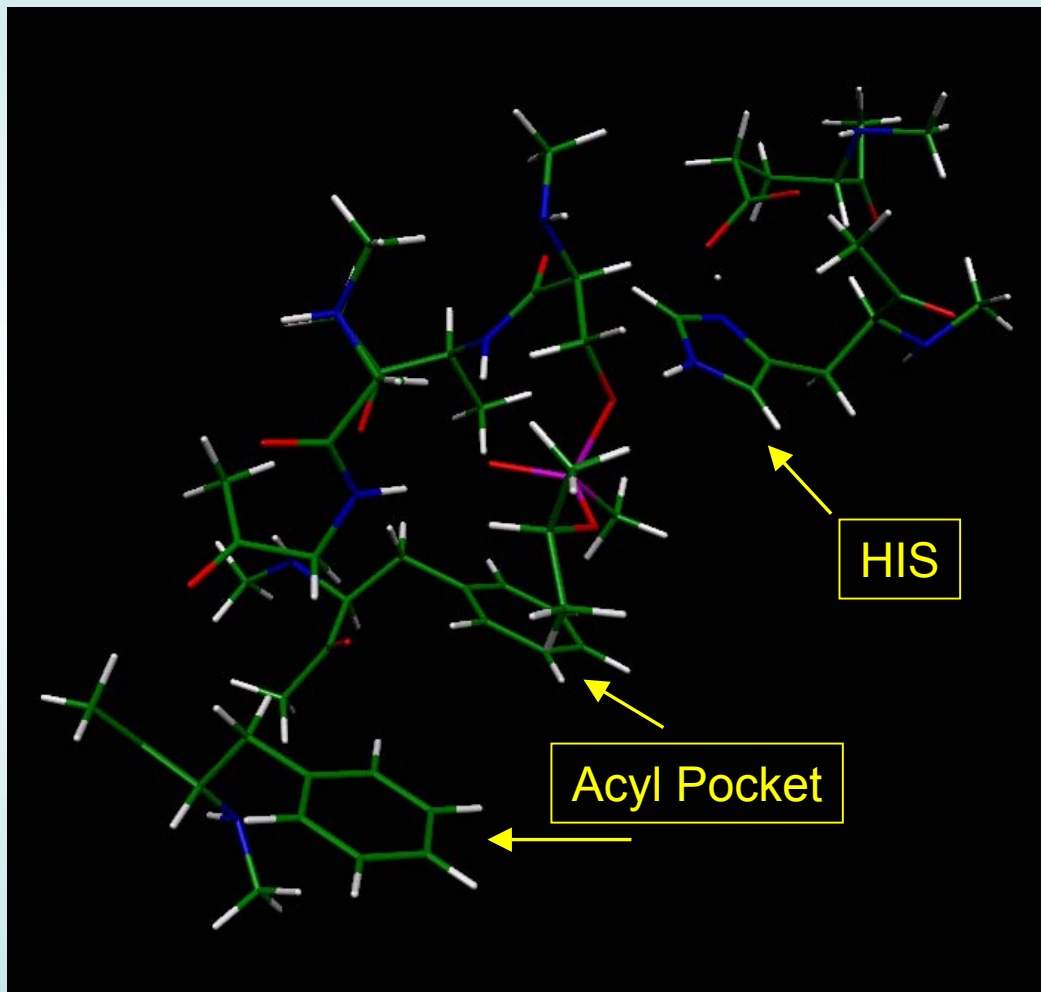




## Still Larger?



B3LYP/3-21G

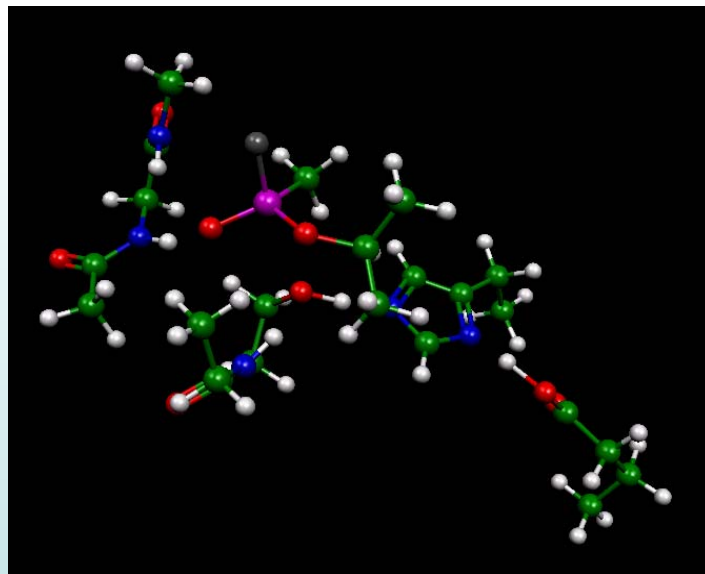
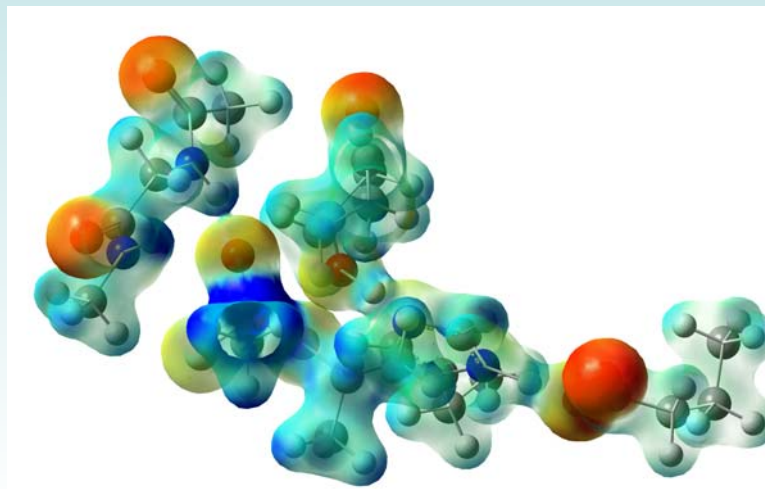


- Acyl Pocket (AP) contribution minimal in
  - reactant
  - product
  - product with LG gone
  - aged product
- No sign of affect on stereoselectivity
- Minimal steric hindrance for iso-propoxy sidechain
- Look at bulkier systems?





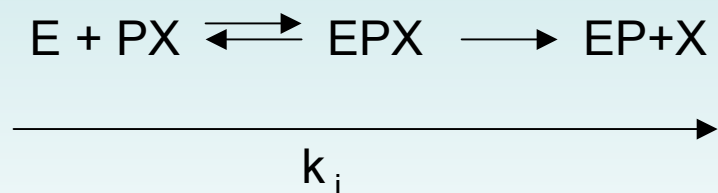
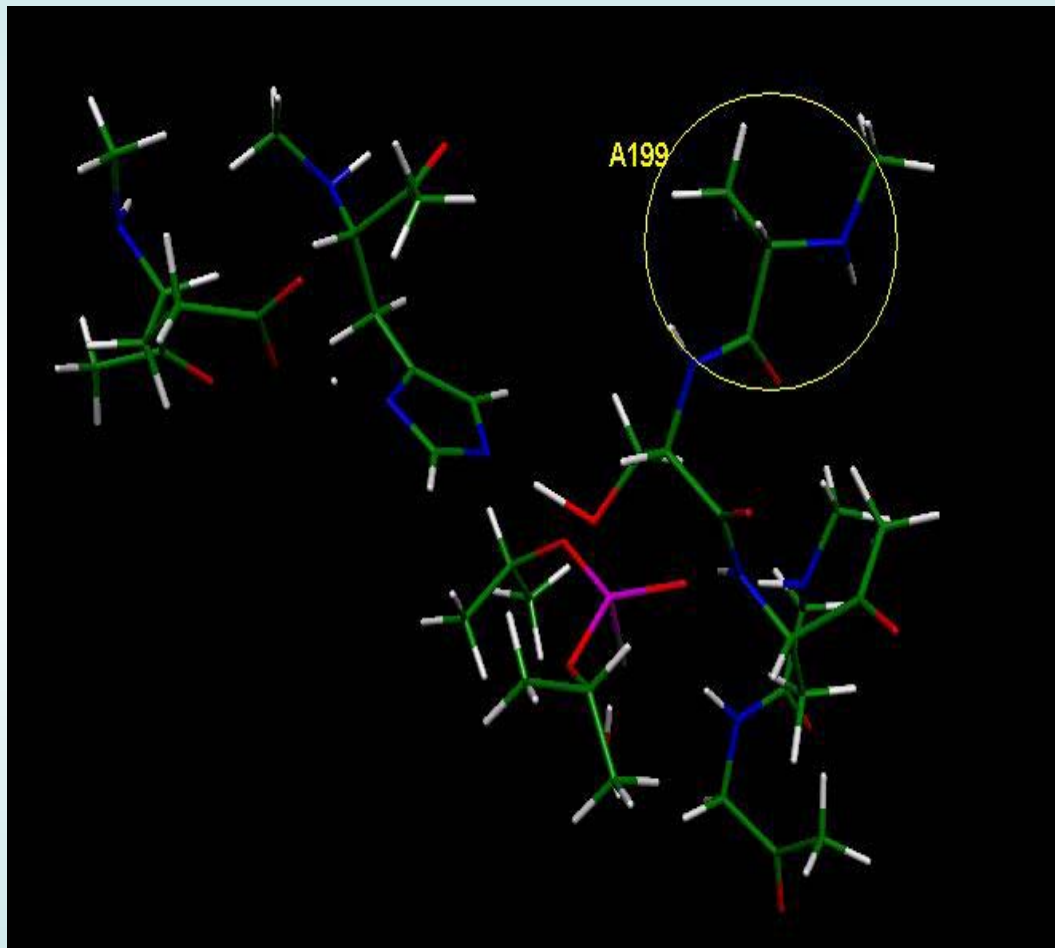
# Chirality



- S product uniformly lower in energy for a variety of OP compounds (varying alkyl sidechains)
- R sarin bound product not isolated
- R reactant (unbound) complex  $\sim 16$  kcal/mol higher in energy than S sarin (bound) product
- Energy difference between enantiomers found even in truncated model (Act + OX)
- P-O orientation into Oxyanion Hole maintained



# Mutagenesis



Exptl evidence of ~15-fold decrease in DFP  $k_i$  with E202A mutation in HuAChE (Ordentlich et al JBC 271 11953 (1996))

EPX complex state for DFP not isolated, energetics underway.

Repeat for DEFP, paraoxon

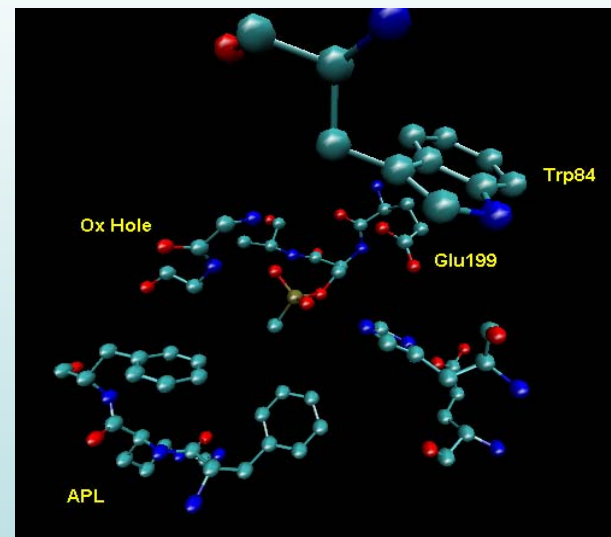
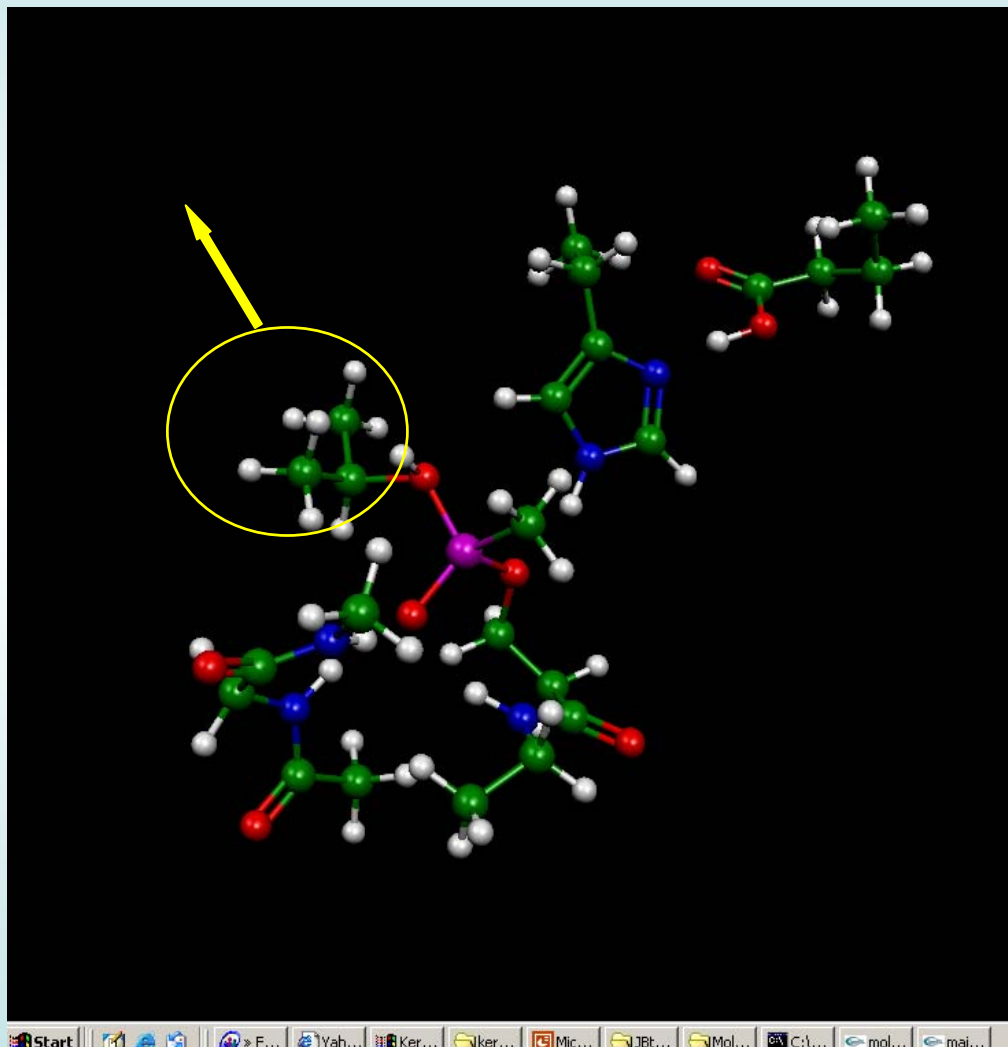


# Aging



B3LYP/3-21G

- Mechanism-transient carbocation vs. push-pull
- Glu199, W84?
- Mapped out high barrier to carbocation mechanism (~40 kcal/mol) w/o proton, repeating with proton

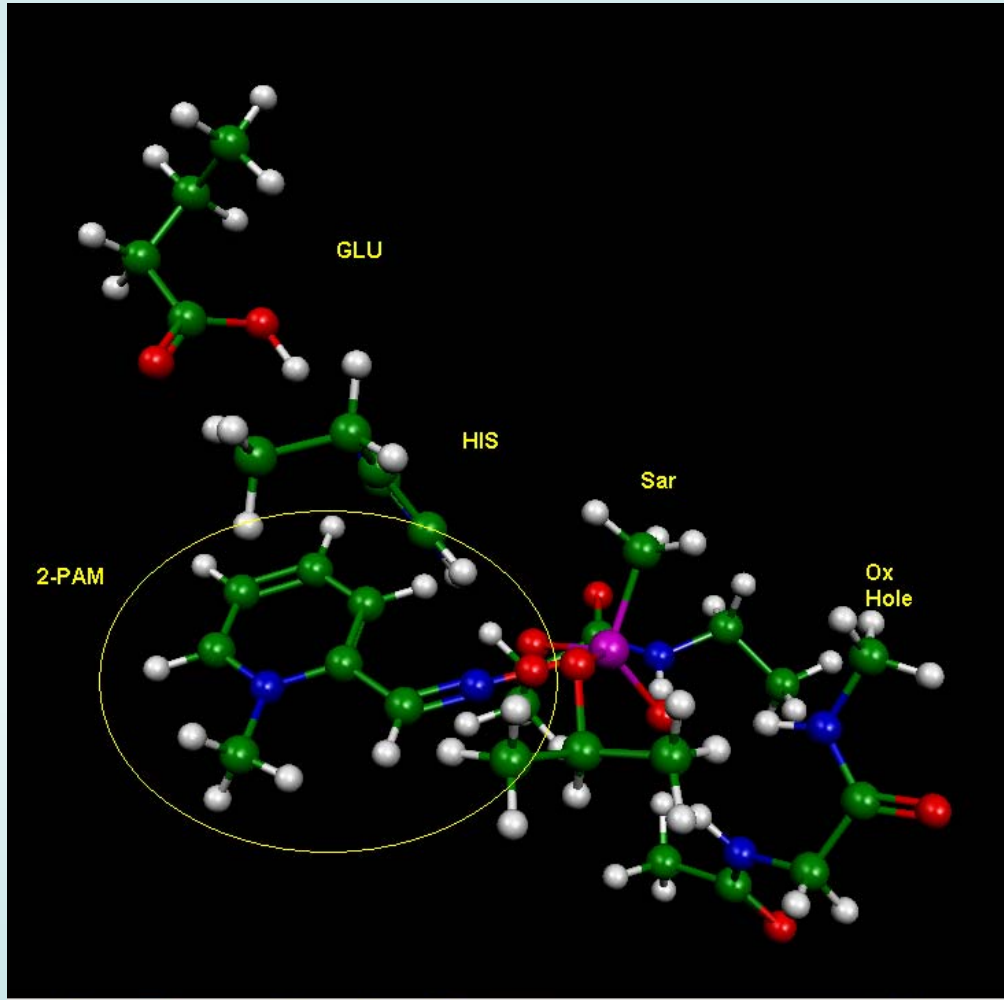


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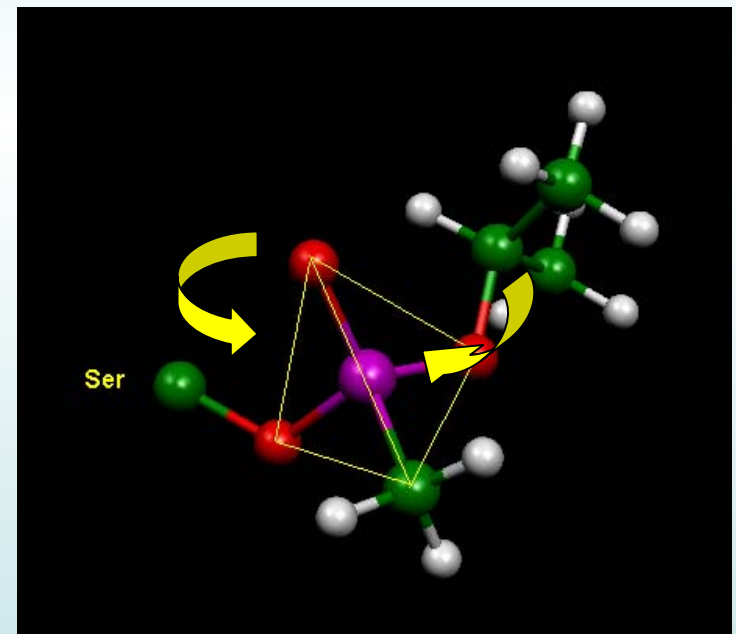


# Reactivators - 2PAM



## Sensitivity to face of attack?

Berman *Structure and Function of Cholinesterases and Related Proteins*  
ed. Doctor *et al.*, Plenum Press, New York, 1998, pp. 413-417.



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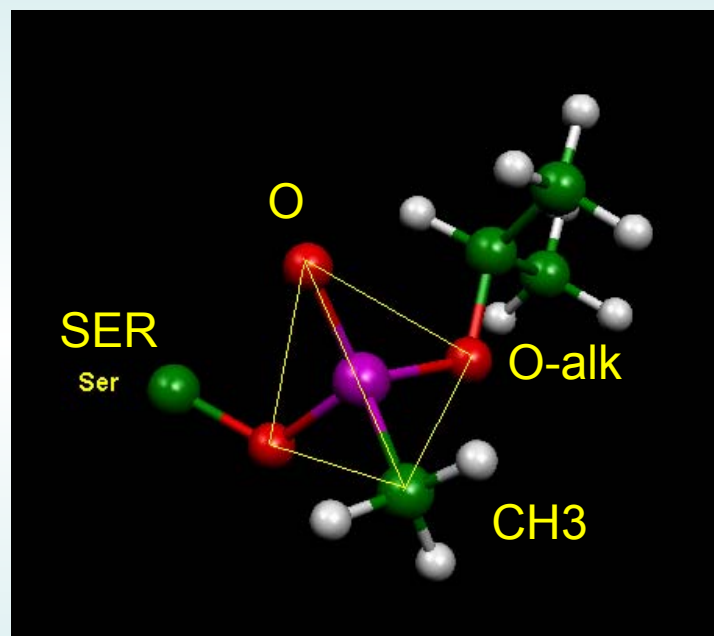
## Reactivators - 2PAM

- SER-Oalk-O face **X**
- CH<sub>3</sub>-Oalk-SER face **X**
- O-Oalk-CH<sub>3</sub> face **X**
- O-Oalk-CH<sub>3</sub> face with H<sub>2</sub>O **X**



Result in -OX in apical position

- Steric hindrance at edge



*I have not failed, I have only  
discovered 10,000 ways that  
do not work. –T.A. Edison*



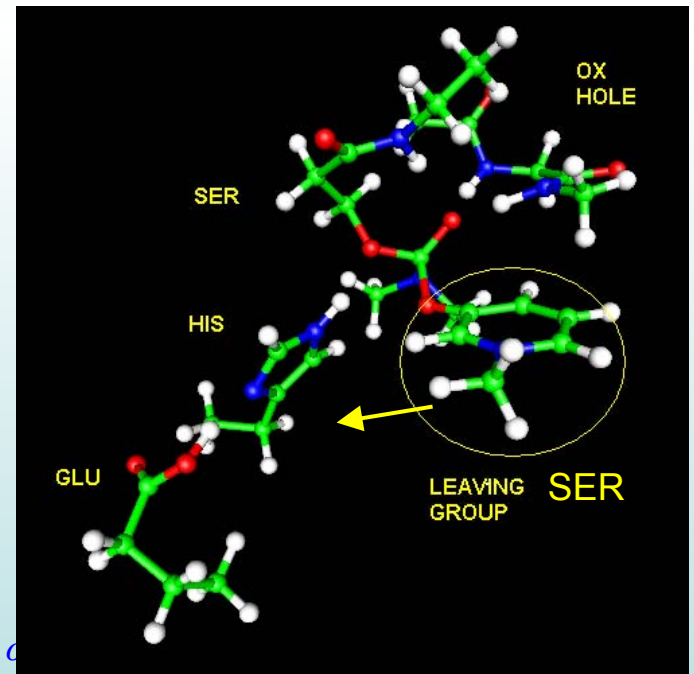
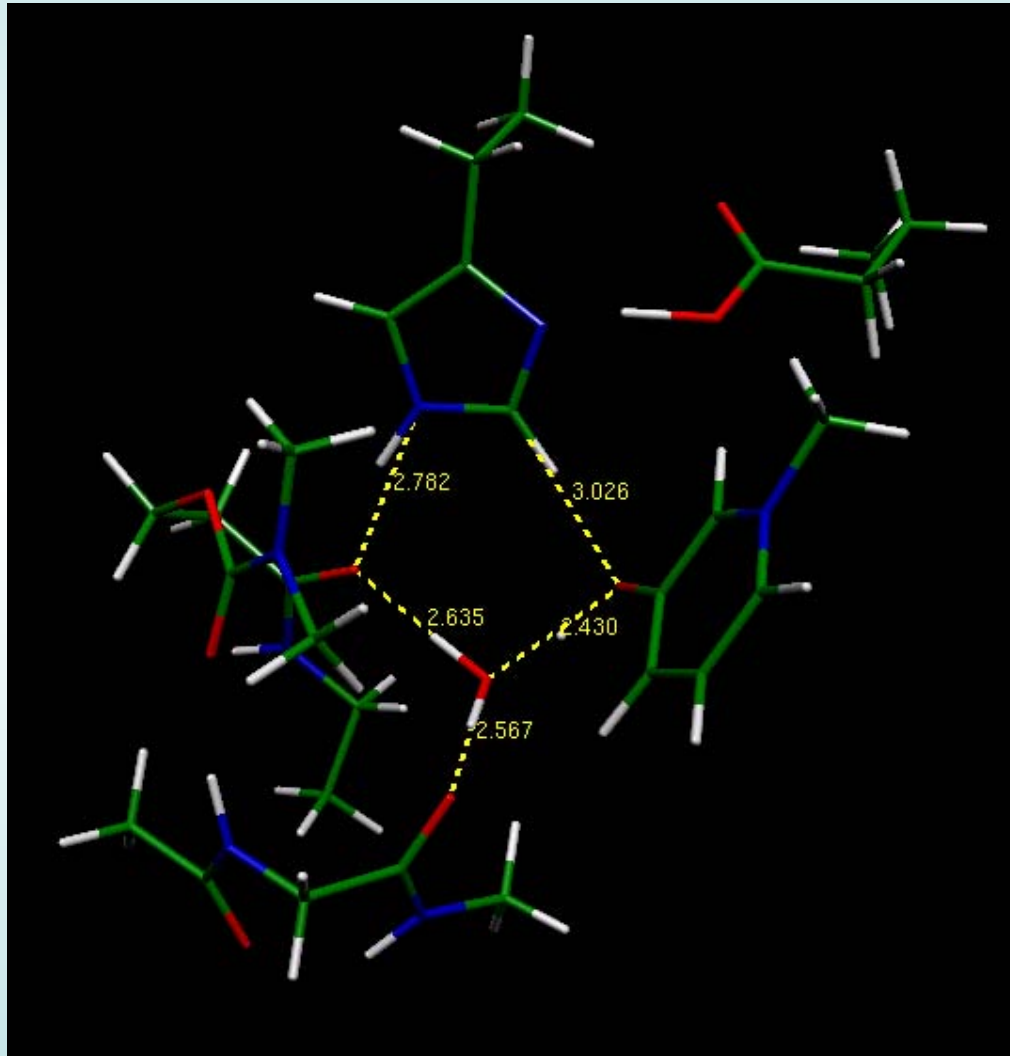
# Prophylaxis

Pyridostigmine

b3lyp 631g(d,p)

Carbamylation of active site  
serine –

- oxanion hole (somewhat)
- role of water again in LG migration
- importance of CHO H-bonds



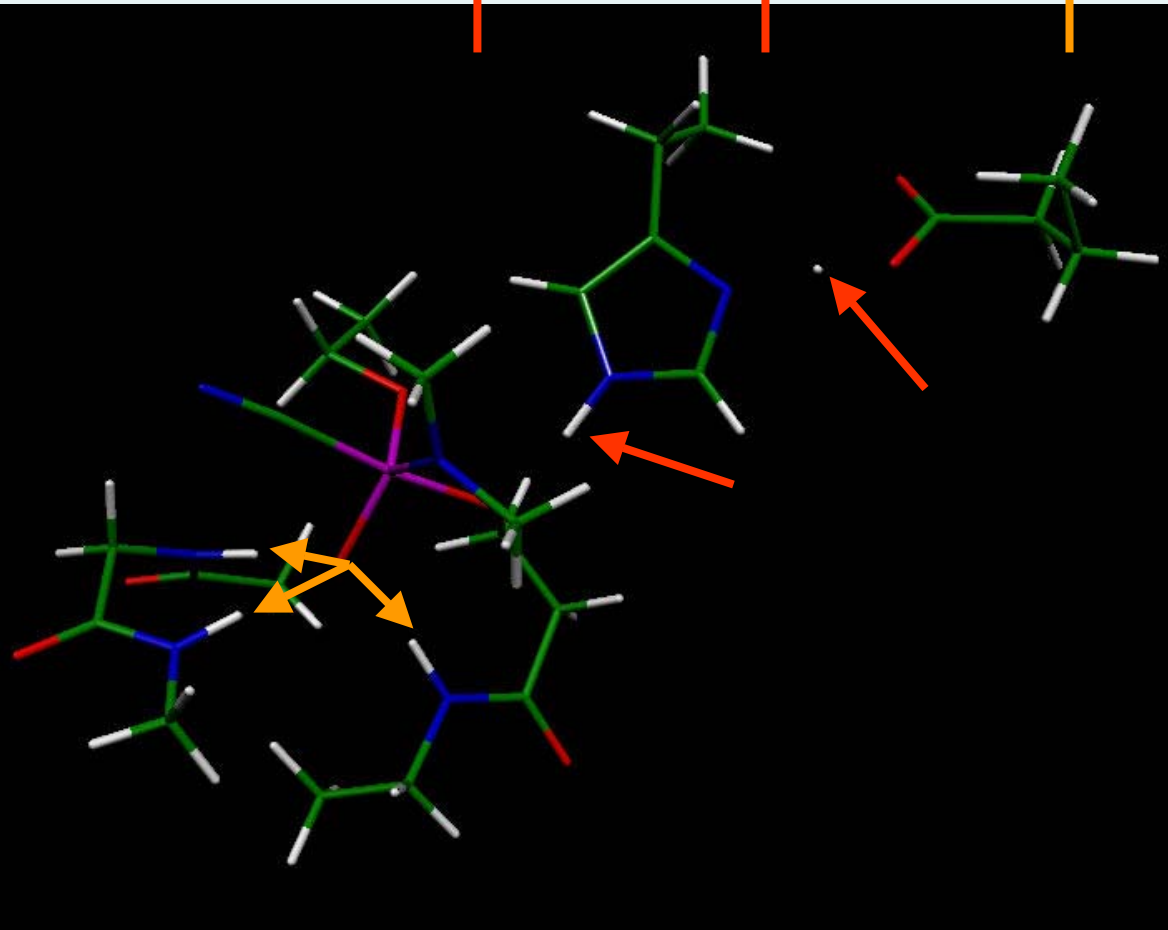
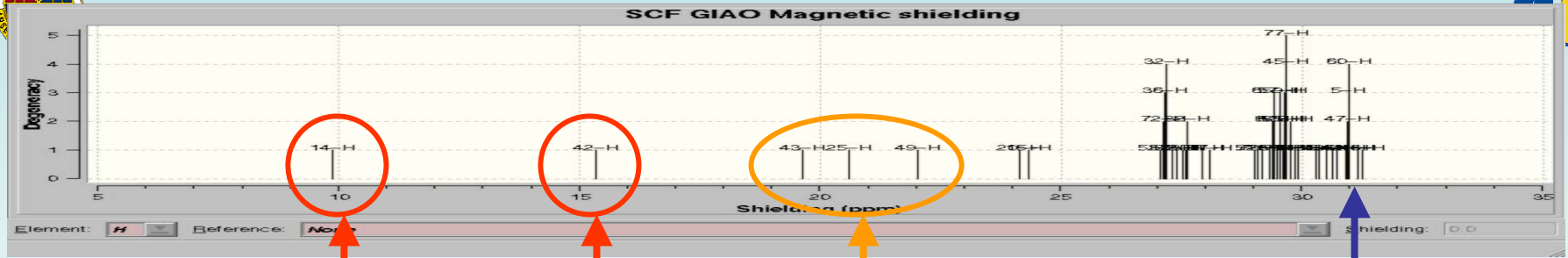
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# SSHB in inhibited enzyme



Calculated proton NMR of bare enzyme b3lyp 6-31g(d,p) and determine shift WRT TSP b3lyp-61g(d,p)

SSHB?

- O-H-N < 2.65 Angstrom

□  $\delta > 15$  ppm





## Calculated Proton NMR shift

# ACTOX

	H1 Shield	H1 dist	H1 angle	H2 Shield	H2 dist	H2 angle	H3 Shield	H3 dist	H4 Shield	H4 dist	H5 Shield	H5 dist
EXPT Massiah et al	14.4 (pH7.5)											
	17.7 (pH 5)	2.62										
bare triad + OX	17.83	2.62	167.20	18.64	2.61	175.80	11.70	2.78	10.65	2.76	7.49	3.04
DFP	22.62	2.53	170.96	16.33	2.62	162.23	11.39	2.81	12.12	2.75	10.93	2.75
DFP w/o F-	18.60	2.61	170.20	11.42	2.79	151.46	8.57	2.87	8.55	3.01	7.86	3.00
DEFP	22.61	2.53	170.96	16.42	2.62	162.65	11.61	2.75	12.05	2.75	10.62	2.83
DMMP	23.36	2.51	171.76	17.72	2.59	164.48	11.99	2.72	12.72	2.73	11.53	2.77



SSHB



Sometimes SSHB



Normal HB



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## Calculated Proton NMR shift

# ACTOX

	H1 Shield	H1 dist	H1 angle	H2 Shield	H2 dist	H2 angle	H3 Shield	H3 dist	H4 Shield	H4 dist	H5 Shield	H5 dist
bare triad + OX	17.83	2.62	167.20	18.64	2.61	175.80	11.70	2.78	10.65	2.76	7.49	3.04
S sarin + glu199	16.27	2.58	166.47	11.65	2.68	175.46	9.16	2.76	2.42	2.94	6.77	2.76
S sarin w/o F-	18.40	2.62	171.72	11.51	2.82	158.40	7.96	2.84	8.75	2.87	8.49	2.91
S sarin	22.34	2.53	170.97	17.12	2.61	172.17	9.54	2.83	12.31	2.75	11.37	2.78
S sarin aged	17.34	2.53	170.63	10.93	2.70	166.24	7.94	2.72	9.08	2.75	7.57	2.80
EXPT (Millard et al)		2.53										
S sarin oniom		2.63	164.64		2.86	137.42		2.53		2.49		2.50
R sarin	23.59	2.51	171.56	19.44	2.53	174.29	9.64	2.77	10.53	3.54	7.63	2.98



SSHB



Sometimes SSHB



Normal HB

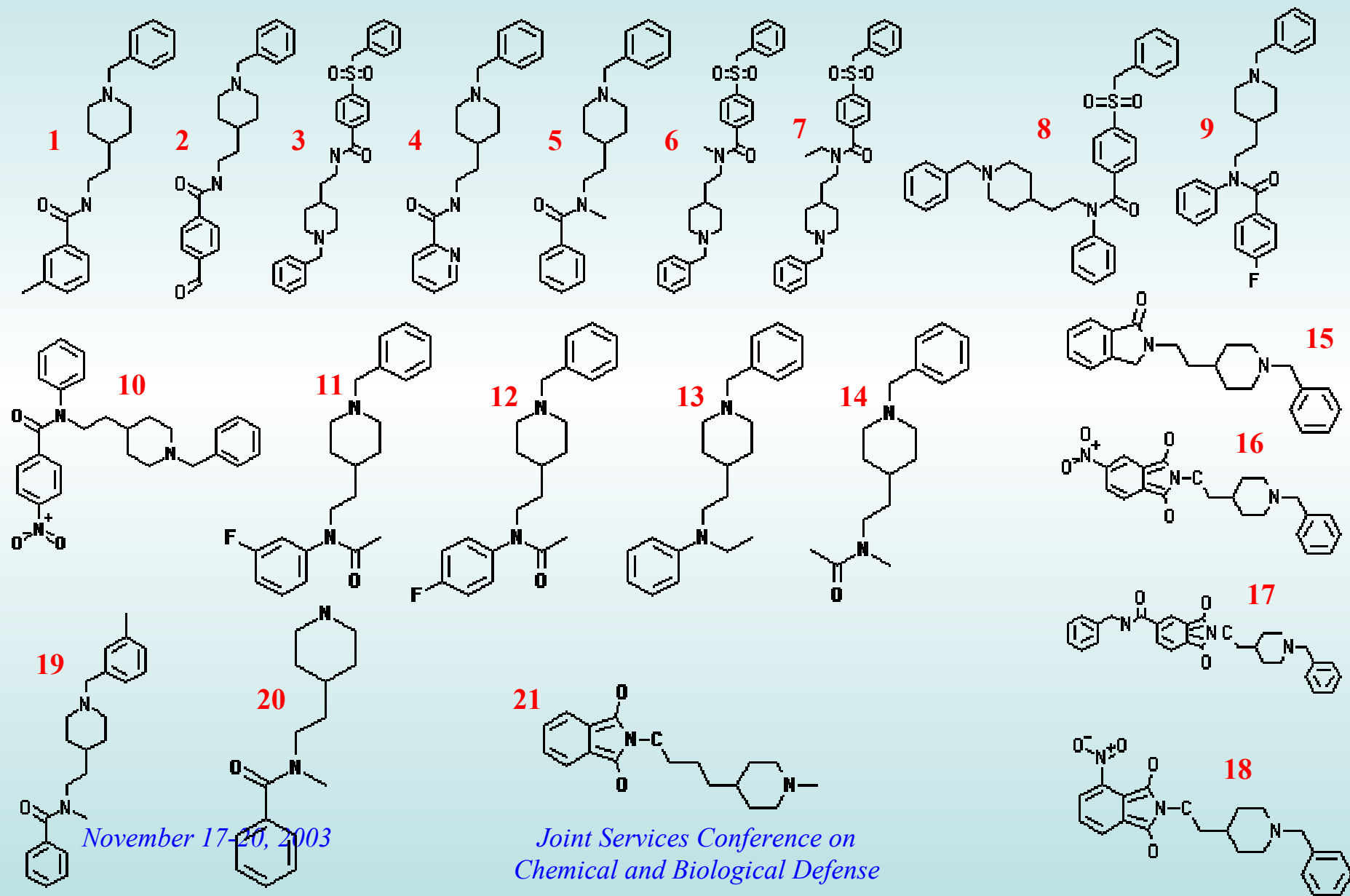


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# Piperidinyl Analogs / Gorge Binders



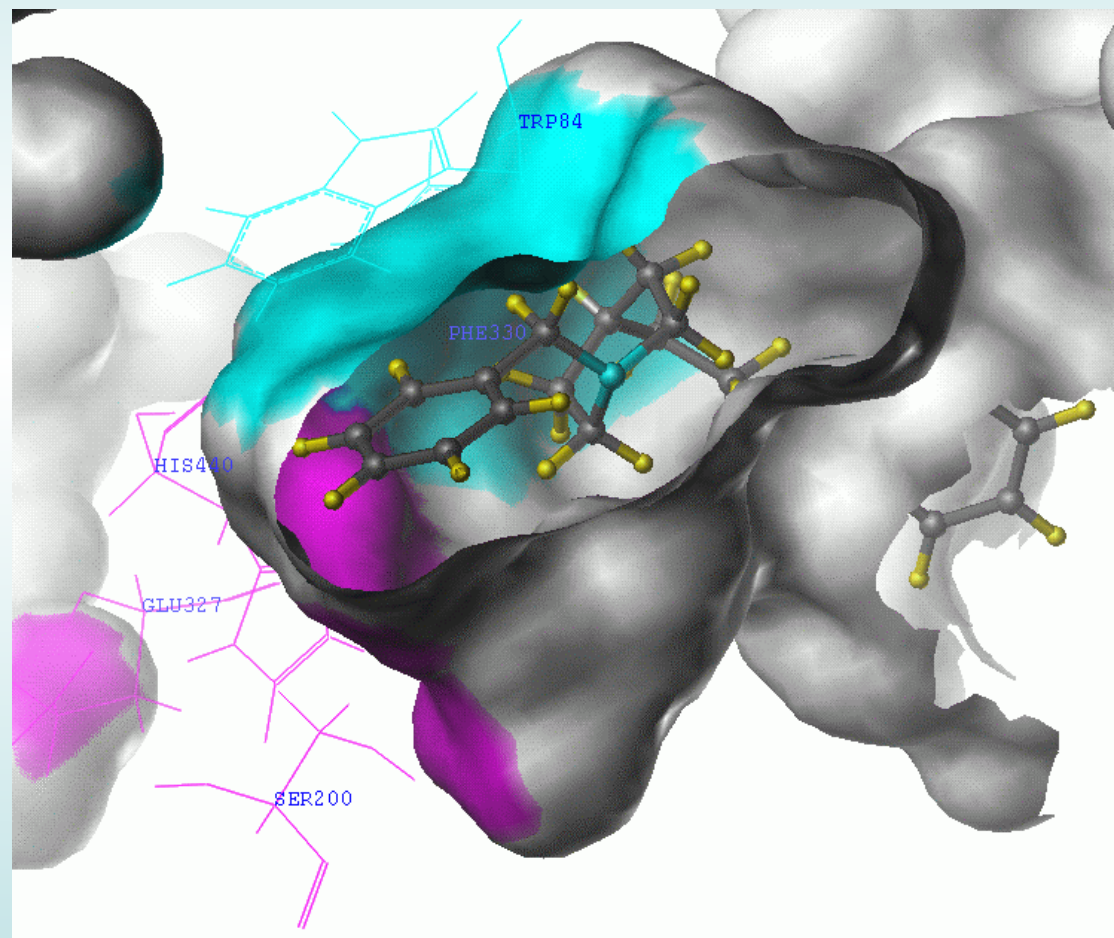
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# Gorge Binders: good correlation

	pIC50(nm)	D_Score
1	6.32790231704712	-141.139999389648
2	6.92081880569458	-153.020004272461
3	7.53760194778442	-169.710006713867
4	6.09690999984741	-130.779998779297
5	6.76955127716064	-141.320007324219
6	9.221848487854	-190.369995117188
7	9.52287864685059	-189.529998779297
8	9.221848487854	-196.570007324219
9	7.74472761154175	-171.0
10	8.26760578155518	-176.869995117188
11	7.18708658218384	-150.380004882812
12	6.68824625015259	-141.970001220703
13	4.92081880569458	-125.790000915527
14	6.18045616149902	-136.619995117188
15	7.00877380371094	-147.160003662109
16	7.90309000015259	-162.320007324219
17	8.65757751464844	-187.289993286133
18	8.04575729370117	-163.059997558594
19	6.83863210678101	-149.080001831055
20	4.58502674102783	-95.4199981689453
21	5.16749095916748	-102.610000610352



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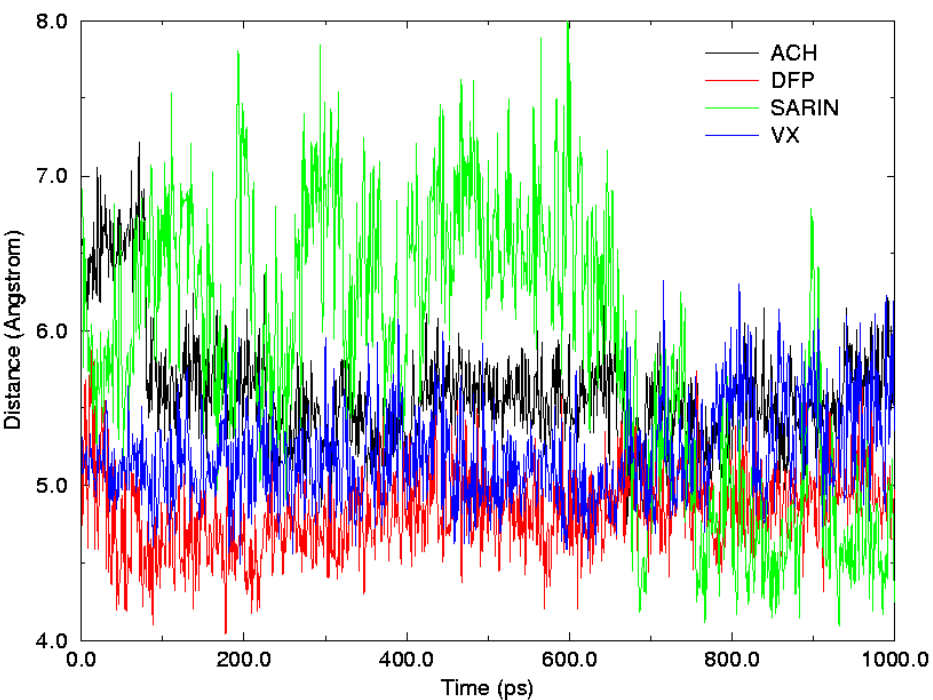
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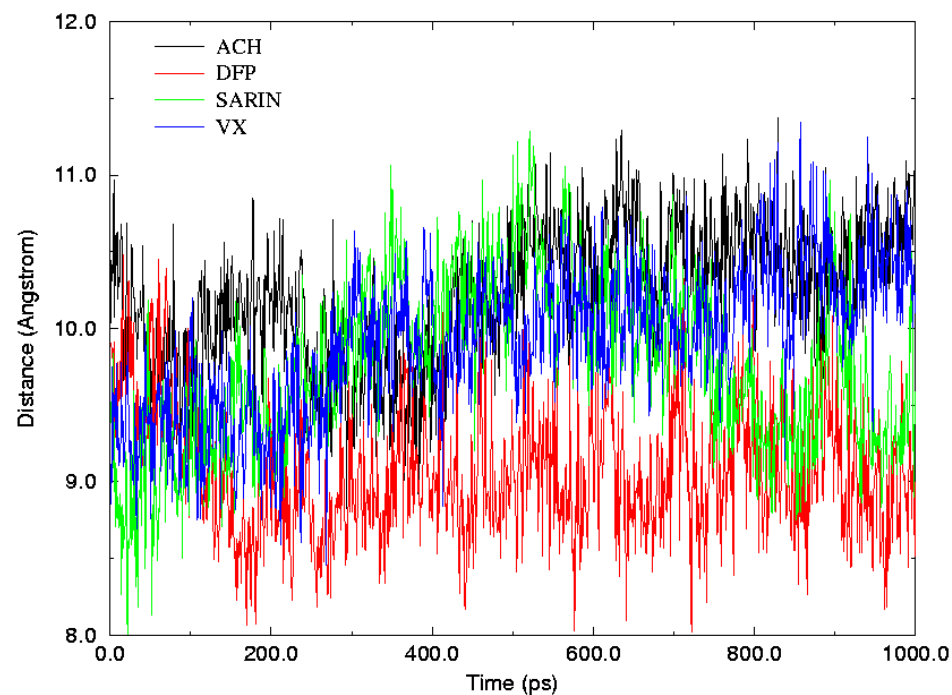
# Gorge vs. Triad Binding



Center of Mass Distance between ligands and Trp84



Center of Mass distance between ligands and His440

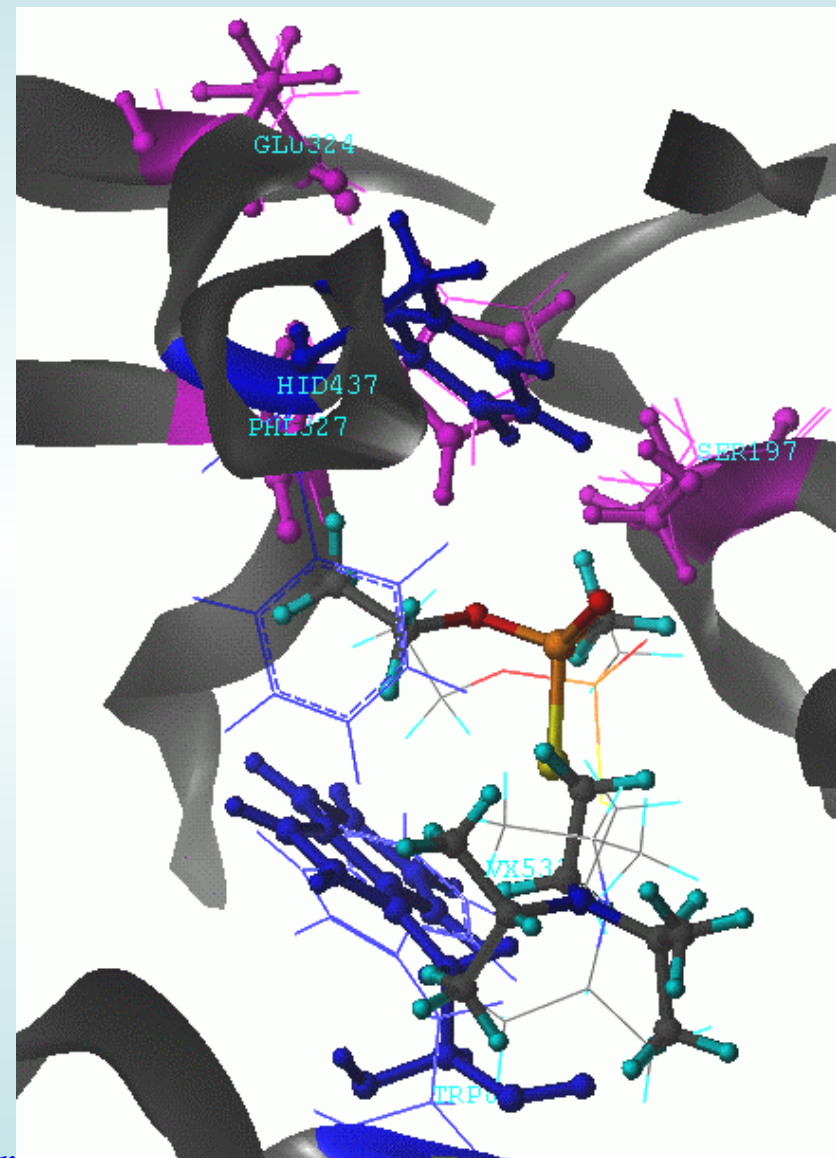
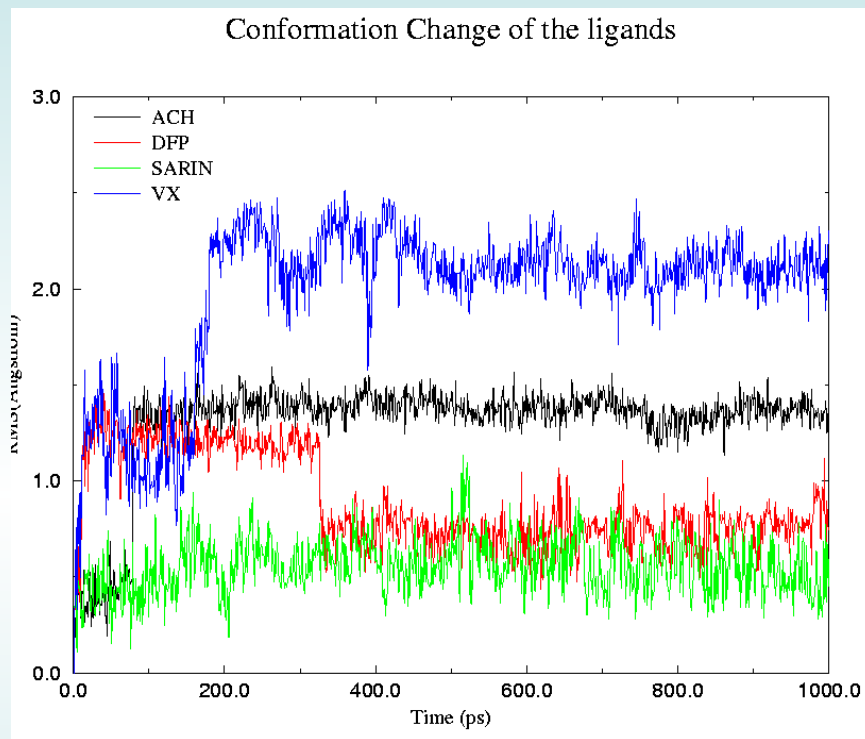


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# Gorge Admission



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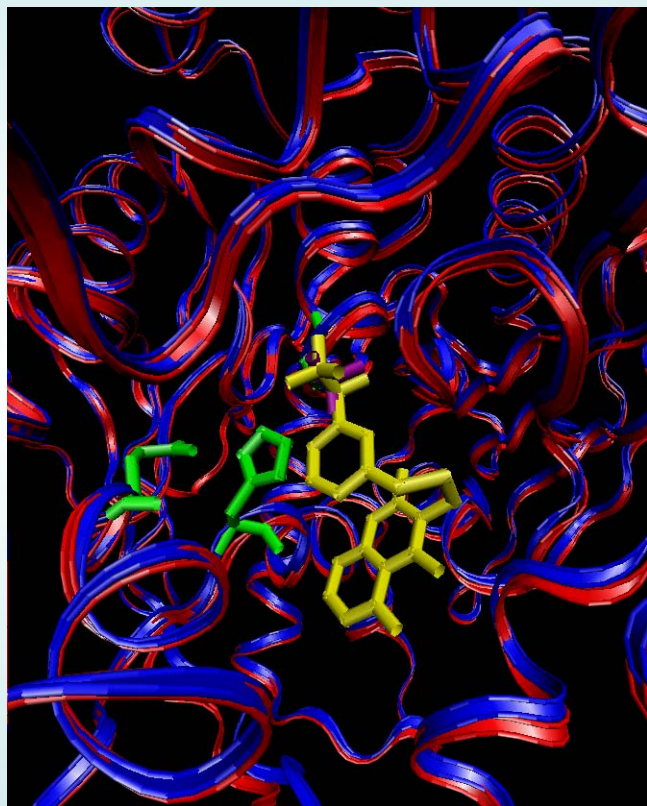
# Conclusions/Future

## Conclusions

- NMR confirmation of SSHB in agreement with expt
- Validated role of oxyanion hole
- Validated Role of solvent and leaving group migration
- Confirmed Stereoselectivity in model

## Ongoing/Future:

- Aging and role of surrounding residues
- Mutagenesis
- Larger systems







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